Application No.: 09/701,586
Inventor: Kock et al.
Reply to Notice of Non-Complaint Amendment of 25 September 2006
Docket No.: 49100

Amendments to the Claims:

1.   (currently amended) An isolated and purified poly(ADP-ribose) polymerase (PARP) homolog comprising human PARP2 (SEQ ID NO: 2) or a functional equivalent thereof which is at least 85% homologous thereto, exhibits poly(ADP-ribose)-synthesizing activity, and has an amino acid sequence which

   a)   has a functional NAD$^+$ binding domain comprising the sequence motif

   PX$_n$(S/T)GX$_3$GKGIYFA (SEQ ID NO:11)

   in which n is an integral value from 1 to 5, and the X radicals are, independently of one another, any amino acid;

and

   b)   lacks a zinc finger sequence motif of the ~~general~~ formula

   CX$_2$CX$_m$HX$_2$C (SEQ ID NO:30)

   in which m is an integral value of 28 or 30, and the X radicals are, independently of one another, any amino acid.

2.   (currently amended) The PARP homolog as claimed in claim 1, wherein the functional NAD$^+$ binding domain comprises ~~one of~~ the following ~~general~~ sequence motif~~s~~:

   (S/T)XGLR(I/V)XPX$_n$(S/T)GX$_3$GKGIYFA (SEQ ID NO:12) ~~or~~

   ~~LLWHG(S/T)X$_7$IL(S/T)XGLR(I/V)XPX$_n$(S/T)GX$_3$GKGIYFAX$_3$SKSAXY (SEQ~~
   ~~ID NO:13)~~

   in which n is an integral value from 1 to 5, and the X radicals are, independently of one another, any amino acid.

3.   (currently amended) The PARP homolog as claimed in claim 1, <u>further</u> comprising ~~at least another one of~~ the ~~following~~ part-sequence motif~~s~~:

   LX$_9$NX$_2$YX$_2$QLLX(D/E)X$_{10/11}$WGRVG (SEQ ID NO: 15)~~,~~

   ~~AX$_3$FXKX$_4$KTXNXWX$_5$FX$_3$PXK (SEQ ID NO:16),~~

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~~QXL(I/L)X$_2$IX$_9$MX$_{10}$PLGKLX$_3$QIX$_6$L (SEQ ID NO:17),~~

~~FYTXIPHXFGX$_3$PP (SEQ ID NO:18); and~~

~~KX$_3$LX$_2$LXDIEXAX$_2$L (SEQ ID NO:19),~~

in which the X radicals are, independently of one another, any amino acid.

4-32.   (canceled)

33.   (new) The PARP homolog as claimed in claim 1, wherein the functional NAD$^+$ binding

domain comprises the following sequence motif:

LLWHG(S/T)X$_7$IL(S/T)XGLR(I/V)XPX$_n$(S/T)GX$_3$GKGIYFAX$_3$SKSAXY (SEQ

ID NO:13)

in which n is an integral value from 1 to 5, and

the X radicals are, independently of one another, any amino acid.

34.   (new) The PARP homolog as claimed in claim 1 further comprising part-sequence motif

AX$_3$FXKX$_4$KTXNXWX$_5$FX$_3$PXK (SEQ ID NO:16)

in which the X radicals are, independently of one another, any amino acid.

35.   (new) The PARP homolog as claimed in claim 1 further comprising part-sequence motif

XL(I/L)X$_2$IX$_9$MX$_{10}$PLGKLX$_3$QIX$_6$L (SEQ ID NO:17)

in which the X radicals are, independently of one another, any amino acid.

36.   (new) The PARP homolog as claimed in claim 1 further comprising part-sequence motif

FYTXIPHXFGX$_3$PP (SEQ ID NO:18)

in which the X radicals are, independently of one another, any amino acid.

37.   (new) The PARP homolog as claimed in claim 1 further comprising part-sequence motif

KX$_3$LX$_2$LXDIEXAX$_2$L (SEQ ID NO:19)

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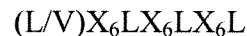in which the X radicals are, independently of one another, any amino acid.

38.   (new) An isolated poly(ADP-ribose) polymerase (PARP) homolog comprising human PARP2 (SEQ ID NO: 2) or a functional equivalent thereof which is at least 85% homologous thereto, exhibits poly(ADP-ribose)-synthesizing activity, and has an amino acid sequence which

a)   has a functional NAD^+ binding domain comprising the sequence motif

$PX_n(S/T)GX_3GKGIYFA$ (SEQ ID NO:11)

in which n is an integral value from 1 to 5, and the X radicals are, independently of one another, any amino acid;

and

b)   lacks a zinc finger sequence motif of the formula

$CX_2CX_mHX_2C$ (SEQ ID NO:30)

in which m is an integral value of 28 or 30, and the X radicals are, independently of one another, any amino acid

further comprising a leucine zipper-like sequence motif:

$(L/V)X_6LX_6LX_6L$

wherein X radicals are, independently of one another, any amino acid.

39.   (new) The PARP homolog as claimed in claim 38 further comprising at least one of the following part-sequence motifs:

$LX_9NX_2YX_2QLLX(D/E)X_{10/11}WGRVG$ (SEQ ID NO: 15),

$AX_3FXKX_4KTXNXWX_5FX_3PXK$ (SEQ ID NO:16),

$QXL(I/L)X_2IX_9MX_{10}PLGKLX_3QIX_6L$ (SEQ ID NO:17),

$FYTXIPHXFGX_3PP$ (SEQ ID NO:18), and

$KX_3LX_2LXDIEXAX_2L$ (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid.

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40. (new) The PARP homolog as claimed in claim 38 further comprising part-sequence motifs:

$LX_9NX_2YX_2QLLX(D/E)X_{10/11}WGRVG$ (SEQ ID NO: 15)

$AX_3FXKX_4KTXNXWX_5FX_3PXK$ (SEQ ID NO:16),

$QXL(I/L)X_2IX_9MX_{10}PLGKLX_3QIX_6L$ (SEQ ID NO:17),

$FYTXIPHXFGX_3PP$ (SEQ ID NO:18), and

$KX_3LX_2LXDIEXAX_2L$ (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid.

41. (new) The PARP homolog as claimed in claim 38 further comprising part-sequence motifs:

$LX_9NX_2YX_2QLLX(D/E)X_{10/11}WGRVG$ (SEQ ID NO: 15)

$AX_3FXKX_4KTXNXWX_5FX_3PXK$ (SEQ ID NO:16),

$QXL(I/L)X_2IX_9MX_{10}PLGKLX_3QIX_6L$ (SEQ ID NO:17),

$FYTXIPHXFGX_3PP$ (SEQ ID NO:18), and

$KX_3LX_2LXDIEXAX_2L$ (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid, wherein

$LX_9NX_2YX_2QLLX(D/E)X_{10/11}WGRVG$

is closest to the N terminus.

42. (new) The PARP homolog as claimed in claim 1 further comprising part-sequence motifs:

$LX_9NX_2YX_2QLLX(D/E)X_{10/11}WGRVG$ (SEQ ID NO: 15)

$AX_3FXKX_4KTXNXWX_5FX_3PXK$ (SEQ ID NO:16),

$QXL(I/L)X_2IX_9MX_{10}PLGKLX_3QIX_6L$ (SEQ ID NO:17),

$FYTXIPHXFGX_3PP$ (SEQ ID NO:18), and

$KX_3LX_2LXDIEXAX_2L$ (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid.

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43.   (new) The PARP homolog as claimed in claim 1 further comprising part-sequence motifs:

$LX_9NX_2YX_2QLLX(D/E)X_{10/11}WGRVG$ (SEQ ID NO: 15)

$AX_3FXKX_4KTXNXWX_5FX_3PXK$ (SEQ ID NO:16),

$QXL(I/L)X_2IX_9MX_{10}PLGKLX_3QIX_6L$ (SEQ ID NO:17),

$FYTXIPHXFGX_3PP$ (SEQ ID NO:18), and

$KX_3LX_2LXDIEXAX_2L$ (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid, wherein

$LX_9NX_2YX_2QLLX(D/E)X_{10/11}WGRVG$

is closest to the N terminus.

44.   (new) The PARP homolog as claimed in claim 1 further comprising at least one of the following:

$GX_3LXVALG$,

$GX2SX_4GX_3PX_aLXGX_2V$, and

$E(Y/F)X_2YXYX_3QXYLL$

in which a is 7 to 9 and

X is any amino acid.

45.   (new) The PARP homolog as claimed in claim 1 further comprising

$GX_3LXEVALG$,

$GX_2SX_4GX_3PX_aLXGX_2V$, and

$E(Y/F)X_2YX_3QX_4YLL$

in which a is 7 to 9 and

X is any amino acid.

46.   (new) The PARP homolog as claimed in claim 1 further comprising

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$GX_3LXEVALG,$

$GX_2SX_4GX_3PX_aLXGX_2V,$ and

$E(Y/F)X_2YX_3QX_4YLL$

in which a is 7 to 9 and

X is any amino acid, wherein

$E(Y/F)X_2YX_3QX_4YLL$

is closest to the C terminus.

47.   (new) An isolated poly(ADP-ribose) polymerase (PARP) homolog comprising human PARP2 (SEQ ID NO: 2) or a functional equivalent thereof which is at least 85% homologous thereto, exhibits poly(ADP-ribose)-synthesizing activity, and has an amino acid sequence which

    a)   has a functional NAD^+ binding domain comprising the sequence motif

        $PX_n(S/T)GX_3GKGIYFA$ (SEQ ID NO:11)

        in which n is an integral value from 1 to 5, and the X radicals are, independently of one another, any amino acid;

    and

    b)   lacks a zinc finger sequence.

48.   (new) The PARP homolog as claimed in claim 47 wherein said PARP lacks a zinc finger sequence motif of the formula

    $CX_2CX_mHX_2C$ (SEQ ID NO:30)

in which m is an integral value of 28 or 30, and

the X radicals are, independently of one another, any amino acid.

49.   (new) The PARP homolog as claimed in claim 47 wherein the functional NAD^+ binding domain comprises the following sequence motif:

    $(S/T)XGLR(I/V)XPX_n(S/T)GX_3GKGIYFA$ (SEQ ID NO:12)

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in which n is an integral value from 1 to 5, and

the X radicals are, independently of one another, any amino acid.

50. (new) The PARP homolog as claimed in claim 47 wherein the functional NAD^+ binding domain comprises the following sequence motif:

$LLWHG(S/T)X_7IL(S/T)XGLR(I/V)XPX_n(S/T)GX_3GKGIYFAX_3SKSAXY$ (SEQ ID NO:13)

in which n is an integral value from 1 to 5, and

the X radicals are, independently of one another, any amino acid.

51. (new) The PARP homolog as claimed in claim 47 further comprising a leucine zipper-like sequence:

$(L/V)X_6LX_6LX_6L$

wherein X radicals are, independently of one another, any amino acid.

52. (new) The PARP homolog as claimed in claim 51 further comprising at least one of the following part-sequence motifs:

$LX_9NX_2YX_2QLLX(D/E)X_{10/11}WGRVG$ (SEQ ID NO: 15),

$AX_3FXKX_4KTXNXWX_5FX_3PXK$ (SEQ ID NO:16),

$QXL(I/L)X_2IX_9MX_{10}PLGKLX_3QIX_6L$ (SEQ ID NO:17),

$FYTXIPHXFGX_3PP$ (SEQ ID NO:18), and

$KX_3LX_2LXDIEXAX_2L$ (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid.

53. (new) The PARP homolog as claimed in claim 51 further comprising:

$LX_9NX_2YX_2QLLX(D/E)X_{10/11}WGRVG$ (SEQ ID NO: 15),

$AX_3FXKX_4KTXNXWX_5FX_3PXK$ (SEQ ID NO:16),

$QXL(I/L)X_2IX_9MX_{10}PLGKLX_3QIX_6L$ (SEQ ID NO:17),

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FYTXIPHXFGX$_3$PP (SEQ ID NO:18), and

KX$_3$LX$_2$LXDIEXAX$_2$L (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid.

54.   (new) The PARP homolog as claimed in claim 51 further comprising:

LX$_9$NX$_2$YX$_2$QLLX(D/E)X$_{10/11}$WGRVG (SEQ ID NO: 15),

AX$_3$FXKX$_4$KTXNXWX$_5$FX$_3$PXK (SEQ ID NO:16),

QXL(I/L)X$_2$IX$_9$MX$_{10}$PLGKLX$_3$QIX$_6$L (SEQ ID NO:17),

FYTXIPHXFGX$_3$PP (SEQ ID NO:18), and

KX$_3$LX$_2$LXDIEXAX$_2$L (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid, wherein

LX$_9$NX$_2$YX$_2$QLLX(D/E)X$_{10/11}$WGRVG

is closest to the N terminus.

55.   (new) The PARP homolog as claimed in claim 47 further comprising at least one of the following:

GX$_3$LXVALG,

GX2SX$_4$GX$_3$PX$_a$LXGX$_2$V, and

E(Y/F)X$_2$YX$_3$QX$_4$YLL

in which a is 7 to 9 and

X is any amino acid.

56.   (new) The PARP homolog as claimed in claim 47 further comprising

GX$_3$LXEVALG,

GX$_2$SX$_4$GX$_3$PX$_a$LXGX$_2$V, and

E(Y/F)X$_2$YX$_3$QX$_4$YLL

in which a is 7 to 9 and

X is any amino acid.

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57. (new) The PARP homolog as claimed in claim 47 further comprising

$GX_3LXEVALG$,

$GX_2SX_4GX_3PX_aLXGX_2V$, and

$E(Y/F)X_2YX_3QX_4YLL$

in which a is 7 to 9 and

X is any amino acid, wherein

$E(Y/F)X_2YX_3QX_4YLL$

is closest to the C terminus.

58. (new) The PARP homolog as claimed in claim 51 further comprising at least one of the following:

$GX_3LXVALG$,

$GX2SX_4GX_3PX_aLXGX_2V$, and

$E(Y/F)X_2YX_3QX_4YLL$

in which a is 7 to 9 and

X is any amino acid.

59. (new) The PARP homolog as claimed in claim 51 further comprising

$GX_3LXEVALG$,

$GX_2SX_4GX_3PX_aLXGX_2V$, and

$E(Y/F)X_2YX_3QX_4YLL$

in which a is 7 to 9 and

X is any amino acid.

60. (new) The PARP homolog as claimed in claim 51 further comprising

$GX_3LXEVALG$,

$GX_2SX_4GX_3PX_aLXGX_2V$, and

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$E(Y/F)X_2YX_3QX_4YLL$

in which a is 7 to 9 and

X is any amino acid, wherein

$E(Y/F)X_2YX_3QX_4YLL$

is closest to the C terminus.